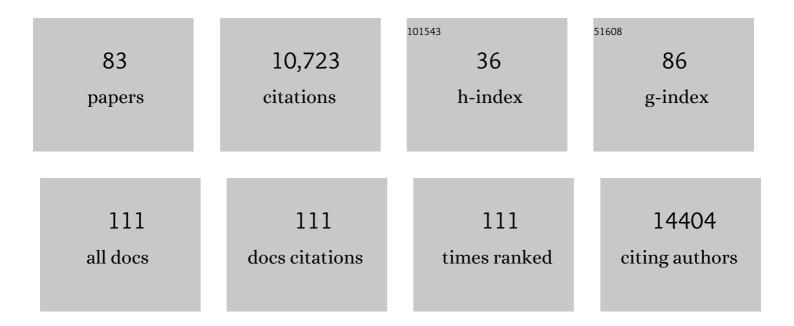
Steven Kelly

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	OrthoFinder: phylogenetic orthology inference for comparative genomics. Genome Biology, 2019, 20, 238.	8.8	3,367
2	OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. Genome Biology, 2015, 16, 157.	8.8	2,812
3	Exon Skipping Is Correlated with Exon Circularization. Journal of Molecular Biology, 2015, 427, 2414-2417.	4.2	308
4	STRIDE: Species Tree Root Inference from Gene Duplication Events. Molecular Biology and Evolution, 2017, 34, 3267-3278.	8.9	192
5	Functional genomics in Trypanosoma brucei: A collection of vectors for the expression of tagged proteins from endogenous and ectopic gene loci. Molecular and Biochemical Parasitology, 2007, 154, 103-109.	1.1	189
6	Deep Evolutionary Comparison of Gene Expression Identifies Parallel Recruitment of Trans-Factors in Two Independent Origins of C4 Photosynthesis. PLoS Genetics, 2014, 10, e1004365.	3.5	165
7	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. Proceedings of the United States of America, 2014, 111, 6672-6677.	7.1	146
8	Clust: automatic extraction of optimal co-expressed gene clusters from gene expression data. Genome Biology, 2018, 19, 172.	8.8	141
9	Reconciling Conflicting Phylogenies in the Origin of Sweet Potato and Dispersal to Polynesia. Current Biology, 2018, 28, 1246-1256.e12.	3.9	133
10	Genomeâ€wide transcript analysis of early maize leaf development reveals gene cohorts associated with the differentiation of <scp><scp>C₄</scp> K</scp> ranz anatomy. Plant Journal, 2013, 75, 656-670.	5.7	120
11	A modular and optimized single marker system for generating <i>Trypanosoma brucei</i> cell lines expressing T7 RNA polymerase and the tetracycline repressor. Open Biology, 2012, 2, 110037.	3.6	117
12	Evolution of GOLDEN2-LIKE gene function in C3 and C4 plants. Planta, 2013, 237, 481-495.	3.2	98
13	Transcriptome, proteome and draft genome of Euglena gracilis. BMC Biology, 2019, 17, 11.	3.8	98
14	The impact of widespread regulatory neofunctionalization on homeolog gene evolution following whole-genome duplication in maize. Genome Research, 2014, 24, 1348-1355.	5.5	94
15	Genome-wide Analysis Reveals Extensive Functional Interaction between DNA Replication Initiation and Transcription in the Genome of Trypanosoma brucei. Cell Reports, 2012, 2, 185-197.	6.4	93
16	Shared origins of a key enzyme during the evolution of C4 and CAM metabolism. Journal of Experimental Botany, 2014, 65, 3609-3621.	4.8	90
17	The Stepwise Increase in the Number of Transcription Factor Families in the Precambrian Predated the Diversification of Plants On Land. Molecular Biology and Evolution, 2016, 33, 2815-2819.	8.9	86
18	Comparative Life Cycle Transcriptomics Revises Leishmania mexicana Genome Annotation and Links a Chromosome Duplication with Parasitism of Vertebrates. PLoS Pathogens, 2015, 11, e1005186.	4.7	85

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19	Phylogenetic trees do not reliably predict feature diversity. Diversity and Distributions, 2014, 20, 600-612.	4.1	83
20	Archaeal phylogenomics provides evidence in support of a methanogenic origin of the Archaea and a thaumarchaeal origin for the eukaryotes. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1009-1018.	2.6	82
21	Installation of C ₄ photosynthetic pathway enzymes in rice using a single construct. Plant Biotechnology Journal, 2021, 19, 575-588.	8.3	78
22	Nitric oxide generated by the rice blast fungus <i>Magnaporthe oryzae</i> drives plant infection. New Phytologist, 2013, 197, 207-222.	7.3	75
23	A taxonomic monograph of Ipomoea integrated across phylogenetic scales. Nature Plants, 2019, 5, 1136-1144.	9.3	67
24	Independent and Parallel Evolution of New Genes by Gene Duplication in Two Origins of C4 Photosynthesis Provides New Insight into the Mechanism of Phloem Loading in C4 Species. Molecular Biology and Evolution, 2016, 33, 1796-1806.	8.9	66
25	Metabolic quirks and the colourful history of the <i>Euglena gracilis</i> secondary plastid. New Phytologist, 2020, 225, 1578-1592.	7.3	65
26	MergeAlign: improving multiple sequence alignment performance by dynamic reconstruction of consensus multiple sequence alignments. BMC Bioinformatics, 2012, 13, 117.	2.6	64
27	Genetic Regulation of the 2D to 3D Growth Transition in the Moss Physcomitrella patens. Current Biology, 2018, 28, 473-478.e5.	3.9	56
28	Dietary nitrogen alters codon bias and genome composition in parasitic microorganisms. Genome Biology, 2016, 17, 226.	8.8	53
29	Phytomonas: Trypanosomatids Adapted to Plant Environments. PLoS Pathogens, 2015, 11, e1004484.	4.7	52
30	Codon choice directs constitutive mRNA levels in trypanosomes. ELife, 2018, 7, .	6.0	52
31	DendroBLAST: Approximate Phylogenetic Trees in the Absence of Multiple Sequence Alignments. PLoS ONE, 2013, 8, e58537.	2.5	52
32	Transcriptional control of photosynthetic capacity: conservation and divergence from <i>Arabidopsis</i> to rice. New Phytologist, 2017, 216, 32-45.	7.3	45
33	Differential Localization of the Two T. brucei Poly(A) Binding Proteins to the Nucleus and RNP Granules Suggests Binding to Distinct mRNA Pools. PLoS ONE, 2013, 8, e54004.	2.5	45
34	Adaptin evolution in kinetoplastids and emergence of the variant surface glycoprotein coat in African trypanosomatids. Molecular Phylogenetics and Evolution, 2013, 67, 123-128.	2.7	44
35	Genome sequencing reveals metabolic and cellular interdependence in an amoeba-kinetoplastid symbiosis. Scientific Reports, 2017, 7, 11688.	3.3	44
36	Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. Current Biology, 2020, 30, 1783-1800.e11.	3.9	42

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37	An Ancestral Role for CONSTITUTIVE TRIPLE RESPONSE1 Proteins in Both Ethylene and Abscisic Acid Signaling. Plant Physiology, 2015, 169, 283-298.	4.8	41
38	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
39	A draft genome for the African crocodilian trypanosome Trypanosoma grayi. Scientific Data, 2014, 1, 140024.	5.3	39
40	Genome organization is a major component of gene expression control in response to stress and during the cell division cycle in <i>trypanosomes</i> . Open Biology, 2012, 2, 120033.	3.6	38
41	Diversification of Function by Different Isoforms of Conventionally Shared RNA Polymerase Subunits. Molecular Biology of the Cell, 2007, 18, 1293-1301.	2.1	37
42	The Amount of Nitrogen Used for Photosynthesis Modulates Molecular Evolution in Plants. Molecular Biology and Evolution, 2018, 35, 1616-1625.	8.9	37
43	Two forward genetic screens for vein density mutants in sorghum converge on a cytochrome P450 gene in the brassinosteroid pathway. Plant Journal, 2015, 84, 257-266.	5.7	36
44	Multiple mechanisms for enhanced plasmodesmata density in disparate subtypes of C4 grasses. Journal of Experimental Botany, 2018, 69, 1135-1145.	4.8	36
45	Rubisco Adaptation Is More Limited by Phylogenetic Constraint Than by Catalytic Trade-off. Molecular Biology and Evolution, 2021, 38, 2880-2896.	8.9	33
46	The molecular evolution of C4 photosynthesis: opportunities for understanding and improving the world's most productive plants. Journal of Experimental Botany, 2019, 70, 795-804.	4.8	32
47	Splicing of many human genes involves sites embedded within introns. Nucleic Acids Research, 2015, 43, 4721-4732.	14.5	31
48	Selection-driven cost-efficiency optimization of transcripts modulates gene evolutionary rate in bacteria. Genome Biology, 2018, 19, 102.	8.8	31
49	An Alternative Strategy for Trypanosome Survival in the Mammalian Bloodstream Revealed through Genome and Transcriptome Analysis of the Ubiquitous Bovine Parasite Trypanosoma (Megatrypanum) theileri. Genome Biology and Evolution, 2017, 9, 2093-2109.	2.5	29
50	C ₄ Photosynthesis in the Rice Paddy: Insights from the Noxious Weed <i>Echinochloa glabrescens</i> . Plant Physiology, 2016, 170, 57-73.	4.8	28
51	SHOOT: phylogenetic gene search and ortholog inference. Genome Biology, 2022, 23, 85.	8.8	28
52	The economics of organellar gene loss and endosymbiotic gene transfer. Genome Biology, 2021, 22, 345.	8.8	28
53	NO GAMETOPHORES 2 Is a Novel Regulator of the 2D to 3D Growth Transition in the Moss Physcomitrella patens. Current Biology, 2021, 31, 555-563.e4.	3.9	27
54	Nuclear pore complex evolution: a trypanosome Mlp analogue functions in chromosomal segregation but lacks transcriptional barrier activity. Molecular Biology of the Cell, 2014, 25, 1421-1436.	2.1	26

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55	Functional <scp>PTB</scp> phosphate transporters are present in streptophyte algae and early diverging land plants. New Phytologist, 2017, 214, 1158-1171.	7.3	25
56	Description of Phytomonas oxycareni n. sp. from the Salivary Glands of Oxycarenus lavaterae. Protist, 2017, 168, 71-79.	1,5	25
57	Identification of a crenarchaeal orthologue of Elf1: implications for chromatin and transcription in Archaea. Biology Direct, 2009, 4, 24.	4.6	23
58	Evolution of the endomembrane systems of trypanosomatids: conservation and specialisation. Journal of Cell Science, 2017, 130, 1421-1434.	2.0	23
59	OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations. BMC Genomics, 2017, 18, 390.	2.8	23
60	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. Genome Biology and Evolution, 2020, 12, 2258-2266.	2.5	23
61	Characterization and Differential Nuclear Localization of Nopp140 and a Novel Nopp140-Like Protein in Trypanosomes. Eukaryotic Cell, 2006, 5, 876-879.	3.4	18
62	Combined Chlorophyll Fluorescence and Transcriptomic Analysis Identifies the P3/P4 Transition as a Key Stage in Rice Leaf Photosynthetic Development. Plant Physiology, 2016, 170, 1655-1674.	4.8	18
63	Candidate regulators of Early Leaf Development in Maize Perturb Hormone Signalling and Secondary Cell Wall Formation When Constitutively Expressed in Rice. Scientific Reports, 2017, 7, 4535.	3.3	18
64	Neofunctionalisation of basic helixâ^'loopâ^'helix proteins occurred when embryophytes colonised the land. New Phytologist, 2019, 223, 993-1008.	7.3	18
65	SLaP mapper: A webserver for identifying and quantifying spliced-leader addition and polyadenylation site usage in kinetoplastid genomes. Molecular and Biochemical Parasitology, 2014, 196, 71-74.	1.1	15
66	Engineering biosynthesis of high-value compounds in photosynthetic organisms. Critical Reviews in Biotechnology, 2017, 37, 779-802.	9.0	15
67	Finding the C4 sweet spot: cellular compartmentation of carbohydrate metabolism in C4 photosynthesis. Journal of Experimental Botany, 2021, 72, 6018-6026.	4.8	14
68	Somatic hybridization provides segregating populations for the identification of causative mutations in sterile mutants of the moss <i>Physcomitrella patens</i> . New Phytologist, 2018, 218, 1270-1277.	7.3	12
69	Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. Current Biology, 2021, 31, 4560-4570.e5.	3.9	12
70	Limited domestic introgression in a final refuge of the wild pigeon. IScience, 2022, 25, 104620.	4.1	11
71	The continuing evolution of publishing in the biological sciences. Biology Open, 2018, 7, .	1.2	10
72	Gene expression data support the hypothesis that Isoetes rootlets are true roots and not modified leaves. Scientific Reports, 2020, 10, 21547.	3.3	9

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73	Subdivision of Light Signaling Networks Contributes to Partitioning of C ₄ Photosynthesis. Plant Physiology, 2020, 182, 1297-1309.	4.8	8
74	Ab Initio Identification of Novel Regulatory Elements in the Genome of Trypanosoma brucei by Bayesian Inference on Sequence Segmentation. PLoS ONE, 2011, 6, e25666.	2.5	8
75	Touching from a distance. Nucleus, 2014, 5, 304-310.	2.2	6
76	OMGene: mutual improvement of gene models through optimisation of evolutionary conservation. BMC Genomics, 2018, 19, 307.	2.8	6
77	Gene Duplication Accelerates the Pace of Protein Gain and Loss from Plant Organelles. Molecular Biology and Evolution, 2020, 37, 969-981.	8.9	6
78	A single <scp>promoterâ€TALE</scp> system for tissueâ€specific and tuneable expression of multiple genes in rice. Plant Biotechnology Journal, 2022, 20, 1786-1806.	8.3	6
79	Transcriptome Sequence of the Bloodstream Form of <i>Trypanoplasma borreli</i> , a Hematozoic Parasite of Fish Transmitted by Leeches. Genome Announcements, 2017, 5, .	0.8	5
80	Genome Sequence of <i>Phytomonas françai</i> , a Cassava (<i>Manihot esculenta</i>) Latex Parasite. Genome Announcements, 2017, 5, .	0.8	5
81	The continuing challenge of paper-mills to publishing in the biological sciences. Biology Open, 2022, 11, .	1.2	3
82	Early-career researchers: answering the most important scientific questions of our time. Biology Open, 2021, 10, .	1.2	2
83	Ten years (and counting) of Biology Open. Biology Open, 2022, 11, .	1.2	1